SEQUENCE LISTING

<110> Altboum, Zeev
    Barry, Eileen M.
    Levine, Myron M.

    University of Maryland

<120> ISOLATION AND CHARACTERIZATION OF THE
  CSA OPERON

<130> UOFMD.006A

<150> 60/198,626
<151> 2000-04-20

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<170> FastSEQ for Windows Version 4.0

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<213> E. coli

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<221> CDS
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gca aat gca aac ttt atg ata tat cca ata tca aaa gat tta aag aat   96
Ala Asn Ala Asn Phe Met Ile Tyr Pro Ile Ser Lys Asp Leu Lys Asn
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gga aat agc gag tta att cgt gtt tat tca aaa tca aaa gag ata caa   144
Gly Asn Ser Glu Leu Ile Arg Val Tyr Ser Lys Ser Lys Glu Ile Gln
            35   40   45

tat ata aaa ata tat aca aaa aag att att aat ccc ggc aca act gaa   192
Tyr Ile Lys Ile Tyr Thr Lys Lys Ile Ile Asn Pro Gly Thr Thr Glu
        50   55   60

gaa cat gaa gtt gat atg ccc aat tgg gat ggt ggg ttt gta gtt act   240
Glu His Glu Val Asp Met Pro Asn Trp Asp Gly Gly Phe Val Val Thr
65   70   75   80

cct caa aaa gtt att ctt cct gca gga ggg agt aaa tca ata cgt tta   288
Pro Gln Lys Val Ile Leu Pro Ala Gly Gly Ser Lys Ser Ile Arg Leu
                85   90   95

act caa ttt aga ata cca aaa aaa gag gaa att tat aga gta tat ttt   336
Thr Gln Phe Arg Ile Pro Lys Lys Glu Glu Ile Tyr Arg Val Tyr Phe
                100   105   110

gag gcg gta aaa cca gat agc aaa gaa aat gta att gat aat aaa aaa   384
Glu Ala Val Lys Pro Asp Ser Lys Glu Asn Val Ile Asp Asn Lys Lys
            115   120   125

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SEQUENCE LISTING

<110> Altboum, Zeev
      Barry, Eileen M.
      Levine, Myron M.

      University of Maryland

<120> ISOLATION AND CHARACTERIZATION OF THE
   CSA OPERON

<130> UOFMD.006A

<150> 60/198,626
<151> 2000-04-20

<160> 40

<170> FastSEQ for Windows Version 4.0

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<220>
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<222> (1)...(717)

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Met His Lys Leu Phe Cys Leu Leu Ser Leu Leu Ile Thr Pro Phe Val
 1   5   10   15

gca aat gca aac ttt atg ata tat cca ata tca aaa gat tta aag aat   96
Ala Asn Ala Asn Phe Met Ile Tyr Pro Ile Ser Lys Asp Leu Lys Asn
            20   25   30

gga aat agc gag tta att cgt gtt tat tca aaa tca aaa gag ata caa   144
Gly Asn Ser Glu Leu Ile Arg Val Tyr Ser Lys Ser Lys Glu Ile Gln
        35   40   45

tat ata aaa ata tat aca aaa aag att att aat ccc ggc aca act gaa   192
Tyr Ile Lys Ile Tyr Thr Lys Lys Ile Ile Asn Pro Gly Thr Thr Glu
    50   55   60

gaa cat gaa gtt gat atg ccc aat tgg gat ggt ggg ttt gta gtt act   240
Glu His Glu Val Asp Met Pro Asn Trp Asp Gly Gly Phe Val Val Thr
65   70   75   80

cct caa aaa gtt att ctt cct gca gga ggg agt aaa tca ata cgt tta   288
Pro Gln Lys Val Ile Leu Pro Ala Gly Gly Ser Lys Ser Ile Arg Leu
                85   90   95

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act caa ttt aga ata cca aaa aaa gag gaa att tat aga gta tat ttt    336
Thr Gln Phe Arg Ile Pro Lys Lys Glu Glu Ile Tyr Arg Val Tyr Phe
            100             105             110

gag gcg gta aaa cca gat agc aaa gaa aat gta att gat aat aaa aaa    384
Glu Ala Val Lys Pro Asp Ser Lys Glu Asn Val Ile Asp Asn Lys Lys
            115             120             125

cta aca aca gag cta tct gtt aat ata att tat gcg gct cta atc aga    432
Leu Thr Thr Glu Leu Ser Val Asn Ile Ile Tyr Ala Ala Leu Ile Arg
        130             135             140

tct tta cca agt gaa caa aac ata tca cta aac att tct aga aat gca    480
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145             150             155             160

aga aaa aat ata att att tat aat aat ggg aat gtt aga gca ggt gtt    528
Arg Lys Asn Ile Ile Ile Tyr Asn Asn Gly Asn Val Arg Ala Gly Val
                165             170             175

aaa gat att tat ttt tgt aag tca tct aat atc gat gat agc tgt gta    576
Lys Asp Ile Tyr Phe Cys Lys Ser Ser Asn Ile Asp Asp Ser Cys Val
            180             185             190

aaa aaa acg cat aac aag aat ata tat cca gaa aag tca ttt gat acg    624
Lys Lys Thr His Asn Lys Asn Ile Tyr Pro Glu Lys Ser Phe Asp Thr
            195             200             205

ctg gtt aat aac aat ttt tct tat gtt ttc att aaa tta aac cat gaa    672
Leu Val Asn Asn Asn Phe Ser Tyr Val Phe Ile Lys Leu Asn His Glu
        210             215             220

gac ata gaa aaa gag caa gga cta ata caa tta aaa gtt cct tga        717
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<213> E. coli

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            20              25              30
Gly Asn Ser Glu Leu Ile Arg Val Tyr Ser Lys Ser Lys Glu Ile Gln
            35              40              45
Tyr Ile Lys Ile Tyr Thr Lys Lys Ile Ile Asn Pro Gly Thr Thr Glu
    50              55              60
Glu His Glu Val Asp Met Pro Asn Trp Asp Gly Gly Phe Val Val Thr
65              70              75              80
Pro Gln Lys Val Ile Leu Pro Ala Gly Gly Ser Lys Ser Ile Arg Leu
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                        85                      90                      95
Thr Gln Phe Arg Ile Pro Lys Lys Glu Glu Ile Tyr Arg Val Tyr Phe
                100                     105                     110
Glu Ala Val Lys Pro Asp Ser Lys Glu Asn Val Ile Asp Asn Lys Lys
                115                     120                     125
Leu Thr Thr Glu Leu Ser Val Asn Ile Ile Tyr Ala Ala Leu Ile Arg
                130                     135                     140
Ser Leu Pro Ser Glu Gln Asn Ile Ser Leu Asn Ile Ser Arg Asn Ala
145                     150                     155                     160
Arg Lys Asn Ile Ile Ile Tyr Asn Asn Gly Asn Val Arg Ala Gly Val
                165                     170                     175
Lys Asp Ile Tyr Phe Cys Lys Ser Ser Asn Ile Asp Asp Ser Cys Val
                180                     185                     190
Lys Lys Thr His Asn Lys Asn Ile Tyr Pro Glu Lys Ser Phe Asp Thr
                195                     200                     205
Leu Val Asn Asn Asn Phe Ser Tyr Val Phe Ile Lys Leu Asn His Glu
                210                     215                     220
Asp Ile Glu Lys Glu Gln Gly Leu Ile Gln Leu Lys Val Pro
225                     230                     235
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 1               5                      10                      15

gta gct atg agt gct tct gca gta gag aaa aat atc act gta aca gct      96
Val Ala Met Ser Ala Ser Ala Val Glu Lys Asn Ile Thr Val Thr Ala
            20                      25                      30

agt gtt gat cct aca att gat att ttg caa gct gat ggt agt agt tta     144
Ser Val Asp Pro Thr Ile Asp Ile Leu Gln Ala Asp Gly Ser Ser Leu
            35                      40                      45

cct act gct gta gaa tta acc tat tca cct gcg gca agt cgt ttt gaa     192
Pro Thr Ala Val Glu Leu Thr Tyr Ser Pro Ala Ala Ser Arg Phe Glu
        50                      55                      60

aat tat aaa atc gca act aaa gtt cat aca aat gtt ata aat aaa aat     240
Asn Tyr Lys Ile Ala Thr Lys Val His Thr Asn Val Ile Asn Lys Asn
 65                     70                      75                      80

gta cta gtt aag ctt gta aat gat cca aaa ctt aca aat gtt ttg gat     288
Val Leu Val Lys Leu Val Asn Asp Pro Lys Leu Thr Asn Val Leu Asp
                    85                      90                      95
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tct aca aaa caa ctc ccc att act gta tca tat gga gga aag act cta    336
Ser Thr Lys Gln Leu Pro Ile Thr Val Ser Tyr Gly Gly Lys Thr Leu
            100             105             110

tca acc gca gat gtg act ttt gaa cct gca gaa tta aat ttt gga acg    384
Ser Thr Ala Asp Val Thr Phe Glu Pro Ala Glu Leu Asn Phe Gly Thr
            115             120             125

tca ggt gta act ggt gta tct tct tcc caa gat tta gtg att ggt gcg    432
Ser Gly Val Thr Gly Val Ser Ser Ser Gln Asp Leu Val Ile Gly Ala
        130             135             140

act aca gca caa gca cca acg gcg gga aat tat agt ggg gtc gtt tct    480
Thr Thr Ala Gln Ala Pro Thr Ala Gly Asn Tyr Ser Gly Val Val Ser
145             150             155             160

atc tta atg acc tta gca tca taa                                    504
Ile Leu Met Thr Leu Ala Ser  *
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Ser Val Asp Pro Thr Ile Asp Ile Leu Gln Ala Asp Gly Ser Ser Leu
            35              40              45
Pro Thr Ala Val Glu Leu Thr Tyr Ser Pro Ala Ala Ser Arg Phe Glu
            50              55              60
Asn Tyr Lys Ile Ala Thr Lys Val His Thr Asn Val Ile Asn Lys Asn
65              70              75              80
Val Leu Val Lys Leu Val Asn Asp Pro Lys Leu Thr Asn Val Leu Asp
                85              90              95
Ser Thr Lys Gln Leu Pro Ile Thr Val Ser Tyr Gly Gly Lys Thr Leu
            100             105             110
Ser Thr Ala Asp Val Thr Phe Glu Pro Ala Glu Leu Asn Phe Gly Thr
            115             120             125
Ser Gly Val Thr Gly Val Ser Ser Ser Gln Asp Leu Val Ile Gly Ala
        130             135             140
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Ile Leu Met Thr Leu Ala Ser
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<213> E. coli

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1               5                   10                  15

cca tat tca gtt ttt tcc gga gat ata ccc aac tct ttc cgt gat tta       96
Pro Tyr Ser Val Phe Ser Gly Asp Ile Pro Asn Ser Phe Arg Asp Leu
            20                  25                  30

tgg gga gaa caa gat gaa ttt tat gaa gta aaa cta tat gga caa act      144
Trp Gly Glu Gln Asp Glu Phe Tyr Glu Val Lys Leu Tyr Gly Gln Thr
            35                  40                  45

cta gga ata cat cga att aaa aca acc cca aca cat att aag ttt tat      192
Leu Gly Ile His Arg Ile Lys Thr Thr Pro Thr His Ile Lys Phe Tyr
        50                  55                  60

tca ccc gaa agc att tta gat aaa ata aat gta aaa aaa gaa aag gaa      240
Ser Pro Glu Ser Ile Leu Asp Lys Ile Asn Val Lys Lys Glu Lys Glu
65                  70                  75                  80

aag aaa ttg agt gtt ttg ttc act aat tct ttt tca aga aat ggc aat      288
Lys Lys Leu Ser Val Leu Phe Thr Asn Ser Phe Ser Arg Asn Gly Asn
                85                  90                  95

atg agt tgt cag ggg aat gct act ata cag tat aac tgc aat tac att      336
Met Ser Cys Gln Gly Asn Ala Thr Ile Gln Tyr Asn Cys Asn Tyr Ile
                100                 105                 110

aaa aca aaa tca gta gat gtc atc gtt gat gat gtt gat aat gtt gtt      384
Lys Thr Lys Ser Val Asp Val Ile Val Asp Asp Val Asp Asn Val Val
            115                 120                 125

aac ctt ttt ata ggt aat gaa ttt ctg gat tct gaa gca cac aat gat      432
Asn Leu Phe Ile Gly Asn Glu Phe Leu Asp Ser Glu Ala His Asn Asp
        130                 135                 140

gaa tat cat caa tta tca cga aat gta aaa aaa gct ttt ata caa agc      480
Glu Tyr His Gln Leu Ser Arg Asn Val Lys Lys Ala Phe Ile Gln Ser
145                 150                 155                 160

cag aca att aat gtc tca gat tct ggg aag tat aaa agt ttg tct gtt      528
Gln Thr Ile Asn Val Ser Asp Ser Gly Lys Tyr Lys Ser Leu Ser Val
                165                 170                 175

tca ggg aat agc gcg ctg ggt att aca gat aca agt tat gct gtc tta      576
Ser Gly Asn Ser Ala Leu Gly Ile Thr Asp Thr Ser Tyr Ala Val Leu
                180                 185                 190

aat tgg tgg atg aat tac aat aaa ttt aat ggt tac agc aac aac gaa      624
```

```
Asn Trp Trp Met Asn Tyr Asn Lys Phe Asn Gly Tyr Ser Asn Asn Glu
    195                 200                 205

aga aca atc aat agt ttg tac ttt aga cat gat tta gat aag aga tat    672
Arg Thr Ile Asn Ser Leu Tyr Phe Arg His Asp Leu Asp Lys Arg Tyr
    210                 215                 220

tat tat caa ttt gga cga atg gat cgt aca gat ttg tca caa agt att    720
Tyr Tyr Gln Phe Gly Arg Met Asp Arg Thr Asp Leu Ser Gln Ser Ile
225                 230                 235                 240

agc ggg aac ttt aat ttt aac tta ctt cct tta ccc gat att gat ggt    768
Ser Gly Asn Phe Asn Phe Asn Leu Leu Pro Leu Pro Asp Ile Asp Gly
                245                 250                 255

ata agg aca gga acc aca caa tct tat atc aaa aat aca gat aag ttt    816
Ile Arg Thr Gly Thr Thr Gln Ser Tyr Ile Lys Asn Thr Asp Lys Phe
                260                 265                 270

atc gca tcc cct gta act gtt atg tta act aat ttt tcc aga gtg gaa    864
Ile Ala Ser Pro Val Thr Val Met Leu Thr Asn Phe Ser Arg Val Glu
                275                 280                 285

gct ttt cgc aat aat caa tta ttg ggc gta tgg tat tta gat tct gga    912
Ala Phe Arg Asn Asn Gln Leu Leu Gly Val Trp Tyr Leu Asp Ser Gly
                290                 295                 300

gta aat gaa tta gat aca gct cgt tta cct tat ggt agt tac gat ctt    960
Val Asn Glu Leu Asp Thr Ala Arg Leu Pro Tyr Gly Ser Tyr Asp Leu
305                 310                 315                 320

aaa tta aaa att ttt gaa aat act cag tta gtt cgt gaa gaa ata att   1008
Lys Leu Lys Ile Phe Glu Asn Thr Gln Leu Val Arg Glu Glu Ile Ile
                325                 330                 335

cct ttt aat aaa ggg aga agt tct att ggt gat atg caa tgg gac gtt   1056
Pro Phe Asn Lys Gly Arg Ser Ser Ile Gly Asp Met Gln Trp Asp Val
                340                 345                 350

ttc att cag gga ggg aat att att aat gac aag gat cgt tac ata gaa   1104
Phe Ile Gln Gly Gly Asn Ile Ile Asn Asp Lys Asp Arg Tyr Ile Glu
                355                 360                 365

aaa caa aat aat cat aag tca tca gtt aat gct ggg cta cgt tta cca   1152
Lys Gln Asn Asn His Lys Ser Ser Val Asn Ala Gly Leu Arg Leu Pro
    370                 375                 380

att acg aaa aat atc tct gtt caa caa gga gca tct gtt ata gat aat   1200
Ile Thr Lys Asn Ile Ser Val Gln Gln Gly Ala Ser Val Ile Asp Asn
385                 390                 395                 400

aaa aat tat tat gaa ggg agt ctc aaa tgg aat tcc ggc att ctg tct   1248
Lys Asn Tyr Tyr Glu Gly Ser Leu Lys Trp Asn Ser Gly Ile Leu Ser
                405                 410                 415
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ggc tca cta aat agt gag ttc agt ttt ctt tgg gga gat aat gca aaa    1296
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ggt aat tat caa agt atc tcg tat acc gat gga ttt agt tta tca ttt    1344
Gly Asn Tyr Gln Ser Ile Ser Tyr Thr Asp Gly Phe Ser Leu Ser Phe
            435             440             445

tat cat aat gat aag cgg gtc gat aat tgt gga aga aat tac aat gct    1392
Tyr His Asn Asp Lys Arg Val Asp Asn Cys Gly Arg Asn Tyr Asn Ala
            450             455             460

ggt tgg agt gga tgc tac gaa tca tat tcg gca tct tta agt att cct    1440
Gly Trp Ser Gly Cys Tyr Glu Ser Tyr Ser Ala Ser Leu Ser Ile Pro
465             470             475             480

tta ttg gga tgg aca agt act ctg gga tat agt gac act tat agt gaa    1488
Leu Leu Gly Trp Thr Ser Thr Leu Gly Tyr Ser Asp Thr Tyr Ser Glu
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tca gtt tat aaa aac cat att ctt tct gaa tat ggt ttt tat aat caa    1536
Ser Val Tyr Lys Asn His Ile Leu Ser Glu Tyr Gly Phe Tyr Asn Gln
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aac ata tat aaa ggg aga acc caa aga tgg caa ctg act tcg tcc acc    1584
Asn Ile Tyr Lys Gly Arg Thr Gln Arg Trp Gln Leu Thr Ser Ser Thr
            515             520             525

tct tta aaa tgg atg gat tat aat ttt atg cca gca att gga ata tat    1632
Ser Leu Lys Trp Met Asp Tyr Asn Phe Met Pro Ala Ile Gly Ile Tyr
            530             535             540

aac agt gag caa aga caa ctg act gat aaa ggc gga tat ata tct gta    1680
Asn Ser Glu Gln Arg Gln Leu Thr Asp Lys Gly Gly Tyr Ile Ser Val
545             550             555             560

act ctc acc cga gcc agc aga gaa aat tca tta aac gca ggg tat tct    1728
Thr Leu Thr Arg Ala Ser Arg Glu Asn Ser Leu Asn Ala Gly Tyr Ser
            565             570             575

tac aac tat tcc aga gga aag tat tct tct aac gaa tta ttt gtt gat    1776
Tyr Asn Tyr Ser Arg Gly Lys Tyr Ser Ser Asn Glu Leu Phe Val Asp
            580             585             590

gga tat atg aca tca aca aat aat ggt gac tat cat gag gta aga atg    1824
Gly Tyr Met Thr Ser Thr Asn Asn Gly Asp Tyr His Glu Val Arg Met
            595             600             605

cgt ttt aat aaa aat aga cat aat gca gaa ggt aga ctt tca ggt cgt    1872
Arg Phe Asn Lys Asn Arg His Asn Ala Glu Gly Arg Leu Ser Gly Arg
            610             615             620

ata aac aat cga ttt gga gat tta aat ggt tca ttc agc atg aat aaa    1920
Ile Asn Asn Arg Phe Gly Asp Leu Asn Gly Ser Phe Ser Met Asn Lys
625             630             635             640
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tcc tca ttt gct ctt aca agt gat gga ttt tac tgg gga gga agt gca      2016
Ser Ser Phe Ala Leu Thr Ser Asp Gly Phe Tyr Trp Gly Gly Ser Ala
                660                 665                 670

tct ggt ttg aca aaa cta gct ggc ggt att atc aag gtt aaa tca aac      2064
Ser Gly Leu Thr Lys Leu Ala Gly Gly Ile Ile Lys Val Lys Ser Asn
                675                 680                 685

gat act aaa aaa aat ctg gta aaa gtg act ggg gca ttg tac ggt gat      2112
Asp Thr Lys Lys Asn Leu Val Lys Val Thr Gly Ala Leu Tyr Gly Asp
    690                 695                 700

tat tcg cta ggg agc aac gat aat gct ttt att cct gta cca gca tta      2160
Tyr Ser Leu Gly Ser Asn Asp Asn Ala Phe Ile Pro Val Pro Ala Leu
705                 710                 715                 720

act cca gcc agt tta att att gaa gat aat aat tat ggt gac aag aat      2208
Thr Pro Ala Ser Leu Ile Ile Glu Asp Asn Asn Tyr Gly Asp Lys Asn
                725                 730                 735

att tct gta ctt gca cca acg aac aac gat atg ttt ata ttg ccg ggt      2256
Ile Ser Val Leu Ala Pro Thr Asn Asn Asp Met Phe Ile Leu Pro Gly
                740                 745                 750

aat gtt tat cct gtt gaa att gaa acc aaa gta agt gtt tct tat att      2304
Asn Val Tyr Pro Val Glu Ile Glu Thr Lys Val Ser Val Ser Tyr Ile
                755                 760                 765

ggt aga ggt ttt gac aaa aac ggc acg cca ctt tct ggc gca cat gtt      2352
Gly Arg Gly Phe Asp Lys Asn Gly Thr Pro Leu Ser Gly Ala His Val
    770                 775                 780

ttg aat gaa cca cat gtt atc ctg gat gag gac ggt gga ttt tcg ttt      2400
Leu Asn Glu Pro His Val Ile Leu Asp Glu Asp Gly Gly Phe Ser Phe
785                 790                 795                 800

gaa tat aca ggt aat gag aaa aca ctt ttt tta tta aag ggc aga act      2448
Glu Tyr Thr Gly Asn Glu Lys Thr Leu Phe Leu Leu Lys Gly Arg Thr
                805                 810                 815

att tat aca tgt caa ctg ggg aaa aat aaa gtt cac aaa ggc att gtt      2496
Ile Tyr Thr Cys Gln Leu Gly Lys Asn Lys Val His Lys Gly Ile Val
                820                 825                 830

ttc gtc gga gat gtt ata tgt gat gtt aat agc aca agt tcc tta cca      2544
Phe Val Gly Asp Val Ile Cys Asp Val Asn Ser Thr Ser Ser Leu Pro
                835                 840                 845

gat gaa ttt gta aag aac cca cgt gtg cag gat ttg ctg gca aag aat      2592
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Asp Lys Gly *
865

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Trp Gly Glu Gln Asp Glu Phe Tyr Glu Val Lys Leu Tyr Gly Gln Thr
        35   40   45
Leu Gly Ile His Arg Ile Lys Thr Thr Pro Thr His Ile Lys Phe Tyr
        50   55   60
Ser Pro Glu Ser Ile Leu Asp Lys Ile Asn Val Lys Lys Glu Lys Glu
65   70   75   80
Lys Lys Leu Ser Val Leu Phe Thr Asn Ser Phe Ser Arg Asn Gly Asn
                85   90   95
Met Ser Cys Gln Gly Asn Ala Thr Ile Gln Tyr Asn Cys Asn Tyr Ile
            100   105   110
Lys Thr Lys Ser Val Asp Val Ile Val Asp Asp Val Asp Asn Val Val
        115   120   125
Asn Leu Phe Ile Gly Asn Glu Phe Leu Asp Ser Glu Ala His Asn Asp
        130   135   140
Glu Tyr His Gln Leu Ser Arg Asn Val Lys Lys Ala Phe Ile Gln Ser
145   150   155   160
Gln Thr Ile Asn Val Ser Asp Ser Gly Lys Tyr Lys Ser Leu Ser Val
                165   170   175
Ser Gly Asn Ser Ala Leu Gly Ile Thr Asp Thr Ser Tyr Ala Val Leu
            180   185   190
Asn Trp Trp Met Asn Tyr Asn Lys Phe Asn Gly Tyr Ser Asn Asn Glu
            195   200   205
Arg Thr Ile Asn Ser Leu Tyr Phe Arg His Asp Leu Asp Lys Arg Tyr
        210   215   220
Tyr Tyr Gln Phe Gly Arg Met Asp Arg Thr Asp Leu Ser Gln Ser Ile
225   230   235   240
Ser Gly Asn Phe Asn Phe Asn Leu Leu Pro Leu Pro Asp Ile Asp Gly
                245   250   255
Ile Arg Thr Gly Thr Thr Gln Ser Tyr Ile Lys Asn Thr Asp Lys Phe
            260   265   270
Ile Ala Ser Pro Val Thr Val Met Leu Thr Asn Phe Ser Arg Val Glu
            275   280   285
Ala Phe Arg Asn Asn Gln Leu Leu Gly Val Trp Tyr Leu Asp Ser Gly
        290   295   300
Val Asn Glu Leu Asp Thr Ala Arg Leu Pro Tyr Gly Ser Tyr Asp Leu
305   310   315   320
Lys Leu Lys Ile Phe Glu Asn Thr Gln Leu Val Arg Glu Glu Ile Ile
                325   330   335

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Pro Phe Asn Lys Gly Arg Ser Ser Ile Gly Asp Met Gln Trp Asp Val
            340             345             350
Phe Ile Gln Gly Gly Asn Ile Ile Asn Asp Lys Asp Arg Tyr Ile Glu
            355             360             365
Lys Gln Asn Asn His Lys Ser Ser Val Asn Ala Gly Leu Arg Leu Pro
            370             375             380
Ile Thr Lys Asn Ile Ser Val Gln Gln Gly Ala Ser Val Ile Asp Asn
385             390             395             400
Lys Asn Tyr Tyr Glu Gly Ser Leu Lys Trp Asn Ser Gly Ile Leu Ser
                405             410             415
Gly Ser Leu Asn Ser Glu Phe Ser Phe Leu Trp Gly Asp Asn Ala Lys
            420             425             430
Gly Asn Tyr Gln Ser Ile Ser Tyr Thr Asp Gly Phe Ser Leu Ser Phe
            435             440             445
Tyr His Asn Asp Lys Arg Val Asp Asn Cys Gly Arg Asn Tyr Asn Ala
450             455             460
Gly Trp Ser Gly Cys Tyr Glu Ser Tyr Ser Ala Ser Leu Ser Ile Pro
465             470             475             480
Leu Leu Gly Trp Thr Ser Thr Leu Gly Tyr Ser Asp Thr Tyr Ser Glu
            485             490             495
Ser Val Tyr Lys Asn His Ile Leu Ser Glu Tyr Gly Phe Tyr Asn Gln
            500             505             510
Asn Ile Tyr Lys Gly Arg Thr Gln Arg Trp Gln Leu Thr Ser Ser Thr
            515             520             525
Ser Leu Lys Trp Met Asp Tyr Asn Phe Met Pro Ala Ile Gly Ile Tyr
            530             535             540
Asn Ser Glu Gln Arg Gln Leu Thr Asp Lys Gly Gly Tyr Ile Ser Val
545             550             555             560
Thr Leu Thr Arg Ala Ser Arg Glu Asn Ser Leu Asn Ala Gly Tyr Ser
            565             570             575
Tyr Asn Tyr Ser Arg Gly Lys Tyr Ser Ser Asn Glu Leu Phe Val Asp
            580             585             590
Gly Tyr Met Thr Ser Thr Asn Asn Gly Asp Tyr His Glu Val Arg Met
            595             600             605
Arg Phe Asn Lys Asn Arg His Asn Ala Glu Gly Arg Leu Ser Gly Arg
            610             615             620
Ile Asn Asn Arg Phe Gly Asp Leu Asn Gly Ser Phe Ser Met Asn Lys
625             630             635             640
Asn Arg Asn Thr Asn Ser Ser Asn His Ser Leu Thr Gly Gly Tyr Asn
            645             650             655
Ser Ser Phe Ala Leu Thr Ser Asp Gly Phe Tyr Trp Gly Gly Ser Ala
            660             665             670
Ser Gly Leu Thr Lys Leu Ala Gly Gly Ile Ile Lys Val Lys Ser Asn
            675             680             685
Asp Thr Lys Lys Asn Leu Val Lys Val Thr Gly Ala Leu Tyr Gly Asp
            690             695             700
Tyr Ser Leu Gly Ser Asn Asp Asn Ala Phe Ile Pro Val Pro Ala Leu
705             710             715             720
Thr Pro Ala Ser Leu Ile Ile Glu Asp Asn Asn Tyr Gly Asp Lys Asn
            725             730             735
Ile Ser Val Leu Ala Pro Thr Asn Asn Asp Met Phe Ile Leu Pro Gly
            740             745             750
Asn Val Tyr Pro Val Glu Ile Glu Thr Lys Val Ser Val Ser Tyr Ile
            755             760             765
Gly Arg Gly Phe Asp Lys Asn Gly Thr Pro Leu Ser Gly Ala His Val
```

```
          770                     775                     780
Leu Asn Glu Pro His Val Ile Leu Asp Glu Asp Gly Gly Phe Ser Phe
785                     790                     795                     800
Glu Tyr Thr Gly Asn Glu Lys Thr Leu Phe Leu Leu Lys Gly Arg Thr
                    805                     810                     815
Ile Tyr Thr Cys Gln Leu Gly Lys Asn Lys Val His Lys Gly Ile Val
                820                     825                     830
Phe Val Gly Asp Val Ile Cys Asp Val Asn Ser Thr Ser Ser Leu Pro
            835                     840                     845
Asp Glu Phe Val Lys Asn Pro Arg Val Gln Asp Leu Leu Ala Lys Asn
        850                     855                     860
Asp Lys Gly
865


<210> 7
<211> 330
<212> DNA
<213> E. coli

<220>
<221> CDS
<222> (1)...(330)

<400> 7
atc agt aag ttg gca gca tca cct gta ttt ctt gaa aga ggg gtg aat      48
Ile Ser Lys Leu Ala Ala Ser Pro Val Phe Leu Glu Arg Gly Val Asn
 1               5                  10                  15

ata tct gta aga ata cag aag caa att tta tca gaa aaa cca tat gtt      96
Ile Ser Val Arg Ile Gln Lys Gln Ile Leu Ser Glu Lys Pro Tyr Val
                20                  25                  30

gca ttc aga ttg aac gga gac ata cta aga cat tta aag gat gca ttg     144
Ala Phe Arg Leu Asn Gly Asp Ile Leu Arg His Leu Lys Asp Ala Leu
            35                  40                  45

atg ata ata tat ggt atg tca aaa ata gat acc aat gat tgt aga aat     192
Met Ile Ile Tyr Gly Met Ser Lys Ile Asp Thr Asn Asp Cys Arg Asn
        50                  55                  60

atg tca agg aaa ata atg aaa aca gaa gtg gat aaa acc tta ctg gat     240
Met Ser Arg Lys Ile Met Lys Thr Glu Val Asp Lys Thr Leu Leu Asp
65                  70                  75                  80

gta tta aaa aat ata aat agc tat gat gac tca gct ttt ata tct aat     288
Val Leu Lys Asn Ile Asn Ser Tyr Asp Asp Ser Ala Phe Ile Ser Asn
                85                  90                  95

ttg ata tat tta att tca aag atc gag aat aat aaa aaa taa           330
Leu Ile Tyr Leu Ile Ser Lys Ile Glu Asn Asn Lys Lys  *
                100                 105
```

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<210> 8
<211> 109
<212> PRT
<213> E. coli

<400> 8
Ile Ser Lys Leu Ala Ala Ser Pro Val Phe Leu Glu Arg Gly Val Asn
1   5   10   15
Ile Ser Val Arg Ile Gln Lys Gln Ile Leu Ser Glu Lys Pro Tyr Val
            20   25   30
Ala Phe Arg Leu Asn Gly Asp Ile Leu Arg His Leu Lys Asp Ala Leu
        35   40   45
Met Ile Ile Tyr Gly Met Ser Lys Ile Asp Thr Asn Asp Cys Arg Asn
    50   55   60
Met Ser Arg Lys Ile Met Lys Thr Glu Val Asp Lys Thr Leu Leu Asp
65   70   75   80
Val Leu Lys Asn Ile Asn Ser Tyr Asp Asp Ser Ala Phe Ile Ser Asn
                85   90   95
Leu Ile Tyr Leu Ile Ser Lys Ile Glu Asn Asn Lys Lys
            100   105

<210> 9
<211> 1086
<212> DNA
<213> E. coli

<220>
<221> CDS
<222> (1)...(1086)

<400> 9
atg aat aag att tta ttt att ttt aca ttg ttt ttc tct tca gta ctt   48
Met Asn Lys Ile Leu Phe Ile Phe Thr Leu Phe Phe Ser Ser Val Leu
1   5   10   15

ttt aca ttt gct gta tcg gca gat aaa att ccc gga gat gaa agc ata   96
Phe Thr Phe Ala Val Ser Ala Asp Lys Ile Pro Gly Asp Glu Ser Ile
                20   25   30

act aat att ttt ggc ccg cgt gac agg aac gaa tct tcc ccc aaa cat   144
Thr Asn Ile Phe Gly Pro Arg Asp Arg Asn Glu Ser Ser Pro Lys His
            35   40   45

aat ata tta aat aac cat att aca gca tac agt gaa agt cat act ctg   192
Asn Ile Leu Asn Asn His Ile Thr Ala Tyr Ser Glu Ser His Thr Leu
        50   55   60

tat gat agg atg act ttt tta tgt ttg tct tct cac aat aca ctt aat   240
Tyr Asp Arg Met Thr Phe Leu Cys Leu Ser Ser His Asn Thr Leu Asn
65   70   75   80

gga gca tgt cca acc agt gag aat cct agc agt tca tcg gtc agc ggt   288
Gly Ala Cys Pro Thr Ser Glu Asn Pro Ser Ser Ser Ser Val Ser Gly
                85   90   95

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```
gaa aca aat ata aca tta caa ttt acg gaa aaa aga agt tta ata aaa      336
Glu Thr Asn Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys
            100                 105                 110

aga gag cta caa att aaa ggc tat aaa caa tta ttg ttc aaa agt gtt      384
Arg Glu Leu Gln Ile Lys Gly Tyr Lys Gln Leu Leu Phe Lys Ser Val
            115                 120                 125

aac tgc cca tcc ggc cta aca ctt aac tca gct cat ttt aac tgt aat      432
Asn Cys Pro Ser Gly Leu Thr Leu Asn Ser Ala His Phe Asn Cys Asn
        130                 135                 140

aaa aac gcg gct tca ggt gca agt tta tat tta tat att cct gct ggc      480
Lys Asn Ala Ala Ser Gly Ala Ser Leu Tyr Leu Tyr Ile Pro Ala Gly
145                 150                 155                 160

gaa cta aaa aat ttg cct ttt ggt ggt atc tgg gat gct act ctg aag      528
Glu Leu Lys Asn Leu Pro Phe Gly Gly Ile Trp Asp Ala Thr Leu Lys
                165                 170                 175

tta aga gta aaa aga cga tat agt gag acc tat gga act tac act ata      576
Leu Arg Val Lys Arg Arg Tyr Ser Glu Thr Tyr Gly Thr Tyr Thr Ile
            180                 185                 190

aat atc act att aaa tta act gat aag gga aat att cag ata tgg tta      624
Asn Ile Thr Ile Lys Leu Thr Asp Lys Gly Asn Ile Gln Ile Trp Leu
            195                 200                 205

cct cag ttc aaa agt gac gct cgc gtc gat ctt aac ttg cgt cca act      672
Pro Gln Phe Lys Ser Asp Ala Arg Val Asp Leu Asn Leu Arg Pro Thr
        210                 215                 220

ggt ggg ggc aca tat att gga aga aat tct gtt gat atg tgc ttt tat      720
Gly Gly Gly Thr Tyr Ile Gly Arg Asn Ser Val Asp Met Cys Phe Tyr
225                 230                 235                 240

gat gga tat agt act aac agc agc tct ttg gag ata aga ttt cag gat      768
Asp Gly Tyr Ser Thr Asn Ser Ser Ser Leu Glu Ile Arg Phe Gln Asp
                245                 250                 255

aac aat cct aaa tct gat ggg aaa ttt tat cta agg aaa ata aat gat      816
Asn Asn Pro Lys Ser Asp Gly Lys Phe Tyr Leu Arg Lys Ile Asn Asp
            260                 265                 270

gac acc aaa gaa att gca tat act ttg tca ctt ctc ttg gcg ggt aaa      864
Asp Thr Lys Glu Ile Ala Tyr Thr Leu Ser Leu Leu Leu Ala Gly Lys
            275                 280                 285

agt tta act cca aca aat gga acg tca tta aat att gct gac gca gct      912
Ser Leu Thr Pro Thr Asn Gly Thr Ser Leu Asn Ile Ala Asp Ala Ala
        290                 295                 300

tct ctg gaa aca aac tgg aat aga att aca gct gtc acc atg cca gaa      960
Ser Leu Glu Thr Asn Trp Asn Arg Ile Thr Ala Val Thr Met Pro Glu
```

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atc agt gtt ccg gtg ttg tgt tgg cct gga cgt ttg caa ttg gat gca   1008
Ile Ser Val Pro Val Leu Cys Trp Pro Gly Arg Leu Gln Leu Asp Ala
            325   330   335

aaa gtg gaa aat ccc gag gct gga caa tat atg ggt aat att aat gtt   1056
Lys Val Glu Asn Pro Glu Ala Gly Gln Tyr Met Gly Asn Ile Asn Val
            340   345   350

act ttc aca cca agt agt caa aca ctc tag   1086
Thr Phe Thr Pro Ser Ser Gln Thr Leu *
            355   360

<210> 10
<211> 361
<212> PRT
<213> E. coli

<400> 10
Met Asn Lys Ile Leu Phe Ile Phe Thr Leu Phe Phe Ser Ser Val Leu
 1   5   10   15
Phe Thr Phe Ala Val Ser Ala Asp Lys Ile Pro Gly Asp Glu Ser Ile
            20   25   30
Thr Asn Ile Phe Gly Pro Arg Asp Arg Asn Glu Ser Ser Pro Lys His
            35   40   45
Asn Ile Leu Asn Asn His Ile Thr Ala Tyr Ser Glu Ser His Thr Leu
            50   55   60
Tyr Asp Arg Met Thr Phe Leu Cys Leu Ser Ser His Asn Thr Leu Asn
65   70   75   80
Gly Ala Cys Pro Thr Ser Glu Asn Pro Ser Ser Ser Ser Val Ser Gly
                85   90   95
Glu Thr Asn Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys
            100   105   110
Arg Glu Leu Gln Ile Lys Gly Tyr Lys Gln Leu Leu Phe Lys Ser Val
            115   120   125
Asn Cys Pro Ser Gly Leu Thr Leu Asn Ser Ala His Phe Asn Cys Asn
            130   135   140
Lys Asn Ala Ala Ser Gly Ala Ser Leu Tyr Leu Tyr Ile Pro Ala Gly
145   150   155   160
Glu Leu Lys Asn Leu Pro Phe Gly Gly Ile Trp Asp Ala Thr Leu Lys
                165   170   175
Leu Arg Val Lys Arg Arg Tyr Ser Glu Thr Tyr Gly Thr Tyr Thr Ile
                180   185   190
Asn Ile Thr Ile Lys Leu Thr Asp Lys Gly Asn Ile Gln Ile Trp Leu
                195   200   205
Pro Gln Phe Lys Ser Asp Ala Arg Val Asp Leu Asn Leu Arg Pro Thr
            210   215   220
Gly Gly Gly Thr Tyr Ile Gly Arg Asn Ser Val Asp Met Cys Phe Tyr
225   230   235   240
Asp Gly Tyr Ser Thr Asn Ser Ser Ser Leu Glu Ile Arg Phe Gln Asp
                245   250   255
Asn Asn Pro Lys Ser Asp Gly Lys Phe Tyr Leu Arg Lys Ile Asn Asp
            260   265   270

```
Asp Thr Lys Glu Ile Ala Tyr Thr Leu Ser Leu Leu Leu Ala Gly Lys
        275             280             285
Ser Leu Thr Pro Thr Asn Gly Thr Ser Leu Asn Ile Ala Asp Ala Ala
        290             295             300
Ser Leu Glu Thr Asn Trp Asn Arg Ile Thr Ala Val Thr Met Pro Glu
305             310             315             320
Ile Ser Val Pro Val Leu Cys Trp Pro Gly Arg Leu Gln Leu Asp Ala
            325             330             335
Lys Val Glu Asn Pro Glu Ala Gly Gln Tyr Met Gly Asn Ile Asn Val
            340             345             350
Thr Phe Thr Pro Ser Ser Gln Thr Leu
        355             360


<210> 11
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 11
gttgaccta caattgatat tttgcaagc                                    29

<210> 12
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 12
cgaccccact ataattcccg ccgttggtgc                                  30

<210> 13
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 13
gtgatatgtt ttgttcactt ggtaaagatc                                  30

<210> 14
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer
```

```
<400> 14
ctcatggctc catttgttgc aaatgcaaac tttatg                              36


<210> 15
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 15
gggatcgatc ccggggcggc cgcgggcccg gtaccaggcc ttctagaaag cttgacgtcg   60


<210> 16
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 16
cccgctagcg gcgcgcctcg cgaggatccg tcgacgacgt caagctttct agaaggcctg   60
g                                                                    61

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 17
aagcttgacg tcgtcgacgg                                                20


<210> 18
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 18
cccgctagcg gcgcgcctcg cg                                             22


<210> 19
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
```

<223> PCR Primer

<400> 19
ccgtgctgac tctacacccc cagatg   26

<210> 20
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 20
gcacatagag aggatagtaa cgccg   25

<210> 21
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 21
cggtcattgt tggccgtgcg ctgcc   25

<210> 22
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 22
cacgcagcgc gctgatgcct tccacgcg   28

<210> 23
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 23
catatttgat atctgagata tctgg   25

<210> 24
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<400> 24
tgttgcattc agattgaacg gag   23

<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<400> 25
tattatgatt cataaataca ctgt   24

<210> 26
<211> 50
<212> DNA
<213> Artificial Sequence

<220>

<400> 26
tgtgggtatt tgtttggaca tcgcagcatt aaatataaaa atagcacagg   50

<210> 27
<211> 7239
<212> DNA
<213> E. coli

<220>
<221> CDS
<222> (283)...(999)

<221> CDS
<222> (1028)...(1531)

<221> CDS
<222> (1589)...(4192)

<221> CDS
<222> (4196)...(5281)

<221> CDS
<222> (5790)...(6119)

<400> 27
atatatctta ttgaggaata tcggtgtcat tgagtaccgt taacttaaga taaagaatct 60
gtctggaaat cgcaggacca agaactctca gtacatctgt ggcgataata ttatcgcttc 120
ttatacattc caatatgcag ttcttgtggg tatttgtttg gacatcgcag cattaaatat 180
aaaaatagca caggaggcat aattatttgt ttttactgtc ttattttttt atcccatttt 240
tttttgtttt gatttatctt tgatgaaagc tcaggaggga atatg cat aaa tta ttt 297
                                                  His Lys Leu Phe

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```
tgt tta cta agt tta ctc ata act cca ttt gtt gca aat gca aac ttt    345
Cys Leu Leu Ser Leu Leu Ile Thr Pro Phe Val Ala Asn Ala Asn Phe
 5                   10                  15                  20

atg ata tat cca ata tca aaa gat tta aag aat gga aat agc gag tta    393
Met Ile Tyr Pro Ile Ser Lys Asp Leu Lys Asn Gly Asn Ser Glu Leu
                25                  30                  35

att cgt gtt tat tca aaa tca aaa gag ata caa tat ata aaa ata tat    441
Ile Arg Val Tyr Ser Lys Ser Lys Glu Ile Gln Tyr Ile Lys Ile Tyr
                40                  45                  50

aca aaa aag att att aat ccc ggc aca act gaa gaa cat gaa gtt gat    489
Thr Lys Lys Ile Ile Asn Pro Gly Thr Thr Glu Glu His Glu Val Asp
            55                  60                  65

atg ccc aat tgg gat ggt ggg ttt gta gtt act cct caa aaa gtt att    537
Met Pro Asn Trp Asp Gly Gly Phe Val Val Thr Pro Gln Lys Val Ile
        70                  75                  80

ctt cct gca gga ggg agt aaa tca ata cgt tta act caa ttt aga ata    585
Leu Pro Ala Gly Gly Ser Lys Ser Ile Arg Leu Thr Gln Phe Arg Ile
 85                  90                  95                  100

cca aaa aaa gag gaa att tat aga gta tat ttt gag gcg gta aaa cca    633
Pro Lys Lys Glu Glu Ile Tyr Arg Val Tyr Phe Glu Ala Val Lys Pro
                105                 110                 115

gat agc aaa gaa aat gta att gat aat aaa aaa cta aca aca gag cta    681
Asp Ser Lys Glu Asn Val Ile Asp Asn Lys Lys Leu Thr Thr Glu Leu
                120                 125                 130

tct gtt aat ata att tat gcg gct cta atc aga tct tta cca agt gaa    729
Ser Val Asn Ile Ile Tyr Ala Ala Leu Ile Arg Ser Leu Pro Ser Glu
            135                 140                 145

caa aac ata tca cta aac att tct aga aat gca aga aaa aat ata att    777
Gln Asn Ile Ser Leu Asn Ile Ser Arg Asn Ala Arg Lys Asn Ile Ile
            150                 155                 160

att tat aat aat ggg aat gtt aga gca ggt gtt aaa gat att tat ttt    825
Ile Tyr Asn Asn Gly Asn Val Arg Ala Gly Val Lys Asp Ile Tyr Phe
165                 170                 175                 180

tgt aag tca tct aat atc gat gat agc tgt gta aaa aaa acg cat aac    873
Cys Lys Ser Ser Asn Ile Asp Asp Ser Cys Val Lys Lys Thr His Asn
                185                 190                 195

aag aat ata tat cca gaa aag tca ttt gat acg ctg gtt aat aac aat    921
Lys Asn Ile Tyr Pro Glu Lys Ser Phe Asp Thr Leu Val Asn Asn Asn
                200                 205                 210

ttt tct tat gtt ttc att aaa tta aac cat gaa gac ata gaa aaa gag    969
```

```
Phe Ser Tyr Val Phe Ile Lys Leu Asn His Glu Asp Ile Glu Lys Glu
        215                 220                 225


caa gga cta ata caa tta aaa gtt cct tga tta ctcatctata tactaaggag 1022
Gln Gly Leu Ile Gln Leu Lys Val Pro  *  Leu
        230                 235


ttctaatgaa attaaaaaaa actattggtg caatg gca ctg acc aca atg ttt    1075
                                        Ala Leu Thr Thr Met Phe
                                                    240


gta gct atg agt gct tct gca gta gag aaa aat atc act gta aca gct   1123
Val Ala Met Ser Ala Ser Ala Val Glu Lys Asn Ile Thr Val Thr Ala
245                 250                 255                 260


agt gtt gat cct aca att gat att ttg caa gct gat ggt agt agt tta   1171
Ser Val Asp Pro Thr Ile Asp Ile Leu Gln Ala Asp Gly Ser Ser Leu
                265                 270                 275


cct act gct gta gaa tta acc tat tca cct gcg gca agt cgt ttt gaa   1219
Pro Thr Ala Val Glu Leu Thr Tyr Ser Pro Ala Ala Ser Arg Phe Glu
                280                 285                 290


aat tat aaa atc gca act aaa gtt cat aca aat gtt ata aat aaa aat   1267
Asn Tyr Lys Ile Ala Thr Lys Val His Thr Asn Val Ile Asn Lys Asn
                295                 300                 305


gta cta gtt aag ctt gta aat gat cca aaa ctt aca aat gtt ttg gat   1315
Val Leu Val Lys Leu Val Asn Asp Pro Lys Leu Thr Asn Val Leu Asp
        310                 315                 320


tct aca aaa caa ctc ccc att act gta tca tat gga gga aag act cta   1363
Ser Thr Lys Gln Leu Pro Ile Thr Val Ser Tyr Gly Gly Lys Thr Leu
325                 330                 335                 340


tca acc gca gat gtg act ttt gaa cct gca gaa tta aat ttt gga acg   1411
Ser Thr Ala Asp Val Thr Phe Glu Pro Ala Glu Leu Asn Phe Gly Thr
                345                 350                 355


tca ggt gta act ggt gta tct tct tcc caa gat tta gtg att ggt gcg   1459
Ser Gly Val Thr Gly Val Ser Ser Ser Gln Asp Leu Val Ile Gly Ala
                360                 365                 370


act aca gca caa gca cca acg gcg gga aat tat agt ggg gtc gtt tct   1507
Thr Thr Ala Gln Ala Pro Thr Ala Gly Asn Tyr Ser Gly Val Val Ser
                375                 380                 385


atc tta atg acc tta gca tca taa ata ttttaatata taaaggagca         1554
Ile Leu Met Thr Leu Ala Ser  *  Ile
        390                 395


ggcacactgc tccttattat atggcaataa taaaatg aca aaa aaa aat aca tta  1609
                                        Thr Lys Lys Asn Thr Leu
                                                    400
```

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```
tat ata acg atc atc gca atg cta act cca tat tca gtt ttt tcc gga    1657
Tyr Ile Thr Ile Ile Ala Met Leu Thr Pro Tyr Ser Val Phe Ser Gly
        405             410             415

gat ata ccc aac tct ttc cgt gat tta tgg gga gaa caa gat gaa ttt    1705
Asp Ile Pro Asn Ser Phe Arg Asp Leu Trp Gly Glu Gln Asp Glu Phe
        420             425             430

tat gaa gta aaa cta tat gga caa act cta gga ata cat cga att aaa    1753
Tyr Glu Val Lys Leu Tyr Gly Gln Thr Leu Gly Ile His Arg Ile Lys
435             440             445             450

aca acc cca aca cat att aag ttt tat tca ccc gaa agc att tta gat    1801
Thr Thr Pro Thr His Ile Lys Phe Tyr Ser Pro Glu Ser Ile Leu Asp
            455             460             465

aaa ata aat gta aaa aaa gaa aag gaa aag aaa ttg agt gtt ttg ttc    1849
Lys Ile Asn Val Lys Lys Glu Lys Glu Lys Lys Leu Ser Val Leu Phe
            470             475             480

act aat tct ttt tca aga aat ggc aat atg agt tgt cag ggg aat gct    1897
Thr Asn Ser Phe Ser Arg Asn Gly Asn Met Ser Cys Gln Gly Asn Ala
        485             490             495

act ata cag tat aac tgc aat tac att aaa aca aaa tca gta gat gtc    1945
Thr Ile Gln Tyr Asn Cys Asn Tyr Ile Lys Thr Lys Ser Val Asp Val
        500             505             510

atc gtt gat gat gtt gat aat gtt gtt aac ctt ttt ata ggt aat gaa    1993
Ile Val Asp Asp Val Asp Asn Val Val Asn Leu Phe Ile Gly Asn Glu
515             520             525             530

ttt ctg gat tct gaa gca cac aat gat gaa tat cat caa tta tca cga    2041
Phe Leu Asp Ser Glu Ala His Asn Asp Glu Tyr His Gln Leu Ser Arg
            535             540             545

aat gta aaa aaa gct ttt ata caa agc cag aca att aat gtc tca gat    2089
Asn Val Lys Lys Ala Phe Ile Gln Ser Gln Thr Ile Asn Val Ser Asp
            550             555             560

tct ggg aag tat aaa agt ttg tct gtt tca ggg aat agc gcg ctg ggt    2137
Ser Gly Lys Tyr Lys Ser Leu Ser Val Ser Gly Asn Ser Ala Leu Gly
            565             570             575

att aca gat aca agt tat gct gtc tta aat tgg tgg atg aat tac aat    2185
Ile Thr Asp Thr Ser Tyr Ala Val Leu Asn Trp Trp Met Asn Tyr Asn
        580             585             590

aaa ttt aat ggt tac agc aac aac gaa aga aca atc aat agt ttg tac    2233
Lys Phe Asn Gly Tyr Ser Asn Asn Glu Arg Thr Ile Asn Ser Leu Tyr
595             600             605             610

ttt aga cat gat tta gat aag aga tat tat tat caa ttt gga cga atg    2281
Phe Arg His Asp Leu Asp Lys Arg Tyr Tyr Tyr Gln Phe Gly Arg Met
            615             620             625
```

```
gat cgt aca gat ttg tca caa agt att agc ggg aac ttt aat ttt aac    2329
Asp Arg Thr Asp Leu Ser Gln Ser Ile Ser Gly Asn Phe Asn Phe Asn
            630             635             640

tta ctt cct tta ccc gat att gat ggt ata agg aca gga acc aca caa    2377
Leu Leu Pro Leu Pro Asp Ile Asp Gly Ile Arg Thr Gly Thr Thr Gln
            645             650             655

tct tat atc aaa aat aca gat aag ttt atc gca tcc cct gta act gtt    2425
Ser Tyr Ile Lys Asn Thr Asp Lys Phe Ile Ala Ser Pro Val Thr Val
            660             665             670

atg tta act aat ttt tcc aga gtg gaa gct ttt cgc aat aat caa tta    2473
Met Leu Thr Asn Phe Ser Arg Val Glu Ala Phe Arg Asn Asn Gln Leu
675             680             685             690

ttg ggc gta tgg tat tta gat tct gga gta aat gaa tta gat aca gct    2521
Leu Gly Val Trp Tyr Leu Asp Ser Gly Val Asn Glu Leu Asp Thr Ala
            695             700             705

cgt tta cct tat ggt agt tac gat ctt aaa tta aaa att ttt gaa aat    2569
Arg Leu Pro Tyr Gly Ser Tyr Asp Leu Lys Leu Lys Ile Phe Glu Asn
            710             715             720

act cag tta gtt cgt gaa gaa ata att cct ttt aat aaa ggg aga agt    2617
Thr Gln Leu Val Arg Glu Glu Ile Ile Pro Phe Asn Lys Gly Arg Ser
            725             730             735

tct att ggt gat atg caa tgg gac gtt ttc att cag gga ggg aat att    2665
Ser Ile Gly Asp Met Gln Trp Asp Val Phe Ile Gln Gly Gly Asn Ile
            740             745             750

att aat gac aag gat cgt tac ata gaa aaa caa aat aat cat aag tca    2713
Ile Asn Asp Lys Asp Arg Tyr Ile Glu Lys Gln Asn Asn His Lys Ser
755             760             765             770

tca gtt aat gct ggg cta cgt tta cca att acg aaa aat atc tct gtt    2761
Ser Val Asn Ala Gly Leu Arg Leu Pro Ile Thr Lys Asn Ile Ser Val
            775             780             785

caa caa gga gca tct gtt ata gat aat aaa aat tat tat gaa ggg agt    2809
Gln Gln Gly Ala Ser Val Ile Asp Asn Lys Asn Tyr Tyr Glu Gly Ser
            790             795             800

ctc aaa tgg aat tcc ggc att ctg tct ggc tca cta aat agt gag ttc    2857
Leu Lys Trp Asn Ser Gly Ile Leu Ser Gly Ser Leu Asn Ser Glu Phe
            805             810             815

agt ttt ctt tgg gga gat aat gca aaa ggt aat tat caa agt atc tcg    2905
Ser Phe Leu Trp Gly Asp Asn Ala Lys Gly Asn Tyr Gln Ser Ile Ser
            820             825             830

tat acc gat gga ttt agt tta tca ttt tat cat aat gat aag cgg gtc    2953
Tyr Thr Asp Gly Phe Ser Leu Ser Phe Tyr His Asn Asp Lys Arg Val
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gat aat tgt gga aga aat tac aat gct ggt tgg agt gga tgc tac gaa   3001
Asp Asn Cys Gly Arg Asn Tyr Asn Ala Gly Trp Ser Gly Cys Tyr Glu
                855   860   865

tca tat tcg gca tct tta agt att cct tta ttg gga tgg aca agt act   3049
Ser Tyr Ser Ala Ser Leu Ser Ile Pro Leu Leu Gly Trp Thr Ser Thr
                870   875   880

ctg gga tat agt gac act tat agt gaa tca gtt tat aaa aac cat att   3097
Leu Gly Tyr Ser Asp Thr Tyr Ser Glu Ser Val Tyr Lys Asn His Ile
                885   890   895

ctt tct gaa tat ggt ttt tat aat caa aac ata tat aaa ggg aga acc   3145
Leu Ser Glu Tyr Gly Phe Tyr Asn Gln Asn Ile Tyr Lys Gly Arg Thr
            900   905   910

caa aga tgg caa ctg act tcg tcc acc tct tta aaa tgg atg gat tat   3193
Gln Arg Trp Gln Leu Thr Ser Ser Thr Ser Leu Lys Trp Met Asp Tyr
915   920   925   930

aat ttt atg cca gca att gga ata tat aac agt gag caa aga caa ctg   3241
Asn Phe Met Pro Ala Ile Gly Ile Tyr Asn Ser Glu Gln Arg Gln Leu
                935   940   945

act gat aaa ggc gga tat ata tct gta act ctc acc cga gcc agc aga   3289
Thr Asp Lys Gly Gly Tyr Ile Ser Val Thr Leu Thr Arg Ala Ser Arg
                950   955   960

gaa aat tca tta aac gca ggg tat tct tac aac tat tcc aga gga aag   3337
Glu Asn Ser Leu Asn Ala Gly Tyr Ser Tyr Asn Tyr Ser Arg Gly Lys
                965   970   975

tat tct tct aac gaa tta ttt gtt gat gga tat atg aca tca aca aat   3385
Tyr Ser Ser Asn Glu Leu Phe Val Asp Gly Tyr Met Thr Ser Thr Asn
            980   985   990

aat ggt gac tat cat gag gta aga atg cgt ttt aat aaa aat aga cat   3433
Asn Gly Asp Tyr His Glu Val Arg Met Arg Phe Asn Lys Asn Arg His
 995   1000   1005   1010

aat gca gaa ggt aga ctt tca ggt cgt ata aac aat cga ttt gga gat   3481
Asn Ala Glu Gly Arg Leu Ser Gly Arg Ile Asn Asn Arg Phe Gly Asp
                1015   1020   1025

tta aat ggt tca ttc agc atg aat aaa aac aga aac acc aac agt agc   3529
Leu Asn Gly Ser Phe Ser Met Asn Lys Asn Arg Asn Thr Asn Ser Ser
                1030   1035   1040

aat cat tct ctc act ggt ggt tat aat tcc tca ttt gct ctt aca agt   3577
Asn His Ser Leu Thr Gly Gly Tyr Asn Ser Ser Phe Ala Leu Thr Ser
                1045   1050   1055

gat gga ttt tac tgg gga gga agt gca tct ggt ttg aca aaa cta gct   3625

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Asp Gly Phe Tyr Trp Gly Gly Ser Ala Ser Gly Leu Thr Lys Leu Ala
    1060                1065                1070

ggc ggt att atc aag gtt aaa tca aac gat act aaa aaa aat ctg gta   3673
Gly Gly Ile Ile Lys Val Lys Ser Asn Asp Thr Lys Lys Asn Leu Val
1075                1080                1085                1090

aaa gtg act ggg gca ttg tac ggt gat tat tcg cta ggg agc aac gat   3721
Lys Val Thr Gly Ala Leu Tyr Gly Asp Tyr Ser Leu Gly Ser Asn Asp
                1095                1100                1105

aat gct ttt att cct gta cca gca tta act cca gcc agt tta att att   3769
Asn Ala Phe Ile Pro Val Pro Ala Leu Thr Pro Ala Ser Leu Ile Ile
                    1110                1115                1120

gaa gat aat aat tat ggt gac aag aat att tct gta ctt gca cca acg   3817
Glu Asp Asn Asn Tyr Gly Asp Lys Asn Ile Ser Val Leu Ala Pro Thr
                    1125                1130                1135

aac aac gat atg ttt ata ttg ccg ggt aat gtt tat cct gtt gaa att   3865
Asn Asn Asp Met Phe Ile Leu Pro Gly Asn Val Tyr Pro Val Glu Ile
        1140                1145                1150

gaa acc aaa gta agt gtt tct tat att ggt aga ggt ttt gac aaa aac   3913
Glu Thr Lys Val Ser Val Ser Tyr Ile Gly Arg Gly Phe Asp Lys Asn
1155                1160                1165                1170

ggc acg cca ctt tct ggc gca cat gtt ttg aat gaa cca cat gtt atc   3961
Gly Thr Pro Leu Ser Gly Ala His Val Leu Asn Glu Pro His Val Ile
                1175                1180                1185

ctg gat gag gac ggt gga ttt tcg ttt gaa tat aca ggt aat gag aaa   4009
Leu Asp Glu Asp Gly Gly Phe Ser Phe Glu Tyr Thr Gly Asn Glu Lys
                1190                1195                1200

aca ctt ttt tta tta aag ggc aga act att tat aca tgt caa ctg ggg   4057
Thr Leu Phe Leu Leu Lys Gly Arg Thr Ile Tyr Thr Cys Gln Leu Gly
            1205                1210                1215

aaa aat aaa gtt cac aaa ggc att gtt ttc gtc gga gat gtt ata tgt   4105
Lys Asn Lys Val His Lys Gly Ile Val Phe Val Gly Asp Val Ile Cys
            1220                1225                1230

gat gtt aat agc aca agt tcc tta cca gat gaa ttt gta aag aac cca   4153
Asp Val Asn Ser Thr Ser Ser Leu Pro Asp Glu Phe Val Lys Asn Pro
1235                1240                1245                1250

cgt gtg cag gat ttg ctg gca aag aat gat aaa gga taa acg            4195
Arg Val Gln Asp Leu Leu Ala Lys Asn Asp Lys Gly  *  Thr
                1255                1260

atg aat aag att tta ttt att ttt aca ttg ttt ttc tct tca gta ctt   4243
    Asn Lys Ile Leu Phe Ile Phe Thr Leu Phe Phe Ser Ser Val Leu
        1265                1270                1275
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ttt aca ttt gct gta tcg gca gat aaa att ccc gga gat gaa agc ata    4291
Phe Thr Phe Ala Val Ser Ala Asp Lys Ile Pro Gly Asp Glu Ser Ile
    1280            1285            1290

act aat att ttt ggc ccg cgt gac agg aac gaa tct tcc ccc aaa cat    4339
Thr Asn Ile Phe Gly Pro Arg Asp Arg Asn Glu Ser Ser Pro Lys His
1295            1300            1305            1310

aat ata tta aat aac cat att aca gca tac agt gaa agt cat act ctg    4387
Asn Ile Leu Asn Asn His Ile Thr Ala Tyr Ser Glu Ser His Thr Leu
            1315            1320            1325

tat gat agg atg act ttt tta tgt ttg tct tct cac aat aca ctt aat    4435
Tyr Asp Arg Met Thr Phe Leu Cys Leu Ser Ser His Asn Thr Leu Asn
            1330            1335            1340

gga gca tgt cca acc agt gag aat cct agc agt tca tcg gtc agc ggt    4483
Gly Ala Cys Pro Thr Ser Glu Asn Pro Ser Ser Ser Ser Val Ser Gly
            1345            1350            1355

gaa aca aat ata aca tta caa ttt acg gaa aaa aga agt tta ata aaa    4531
Glu Thr Asn Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys
    1360            1365            1370

aga gag cta caa att aaa ggc tat aaa caa tta ttg ttc aaa agt gtt    4579
Arg Glu Leu Gln Ile Lys Gly Tyr Lys Gln Leu Leu Phe Lys Ser Val
1375            1380            1385            1390

aac tgc cca tcc ggc cta aca ctt aac tca gct cat ttt aac tgt aat    4627
Asn Cys Pro Ser Gly Leu Thr Leu Asn Ser Ala His Phe Asn Cys Asn
            1395            1400            1405

aaa aac gcg gct tca ggt gca agt tta tat tta tat att cct gct ggc    4675
Lys Asn Ala Ala Ser Gly Ala Ser Leu Tyr Leu Tyr Ile Pro Ala Gly
            1410            1415            1420

gaa cta aaa aat ttg cct ttt ggt ggt atc tgg gat gct act ctg aag    4723
Glu Leu Lys Asn Leu Pro Phe Gly Gly Ile Trp Asp Ala Thr Leu Lys
            1425            1430            1435

tta aga gta aaa aga cga tat agt gag acc tat gga act tac act ata    4771
Leu Arg Val Lys Arg Arg Tyr Ser Glu Thr Tyr Gly Thr Tyr Thr Ile
    1440            1445            1450

aat atc act att aaa tta act gat aag gga aat att cag ata tgg tta    4819
Asn Ile Thr Ile Lys Leu Thr Asp Lys Gly Asn Ile Gln Ile Trp Leu
1455            1460            1465            1470

cct cag ttc aaa agt gac gct cgc gtc gat ctt aac ttg cgt cca act    4867
Pro Gln Phe Lys Ser Asp Ala Arg Val Asp Leu Asn Leu Arg Pro Thr
            1475            1480            1485

ggt ggg ggc aca tat att gga aga aat tct gtt gat atg tgc ttt tat    4915
Gly Gly Gly Thr Tyr Ile Gly Arg Asn Ser Val Asp Met Cys Phe Tyr
            1490            1495            1500
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gat gga tat agt act aac agc agc tct ttg gag ata aga ttt cag gat   4963
Asp Gly Tyr Ser Thr Asn Ser Ser Ser Leu Glu Ile Arg Phe Gln Asp
        1505              1510              1515


aac aat cct aaa tct gat ggg aaa ttt tat cta agg aaa ata aat gat   5011
Asn Asn Pro Lys Ser Asp Gly Lys Phe Tyr Leu Arg Lys Ile Asn Asp
        1520              1525              1530


gac acc aaa gaa att gca tat act ttg tca ctt ctc ttg gcg ggt aaa   5059
Asp Thr Lys Glu Ile Ala Tyr Thr Leu Ser Leu Leu Leu Ala Gly Lys
1535              1540              1545              1550


agt tta act cca aca aat gga acg tca tta aat att gct gac gca gct   5107
Ser Leu Thr Pro Thr Asn Gly Thr Ser Leu Asn Ile Ala Asp Ala Ala
             1555              1560              1565


tct ctg gaa aca aac tgg aat aga att aca gct gtc acc atg cca gaa   5155
Ser Leu Glu Thr Asn Trp Asn Arg Ile Thr Ala Val Thr Met Pro Glu
             1570              1575              1580


atc agt gtt ccg gtg ttg tgt tgg cct gga cgt ttg caa ttg gat gca   5203
Ile Ser Val Pro Val Leu Cys Trp Pro Gly Arg Leu Gln Leu Asp Ala
        1585              1590              1595


aaa gtg gaa aat ccc gag gct gga caa tat atg ggt aat att aat gtt   5251
Lys Val Glu Asn Pro Glu Ala Gly Gln Tyr Met Gly Asn Ile Asn Val
        1600              1605              1610


act ttc aca cca agt agt caa aca ctc tag ata acaacaatat tggcgctatt 5304
Thr Phe Thr Pro Ser Ser Gln Thr Leu  *  Ile
1615              1620


gcgcgccaat attgtaaagg ggtaatctgt ttgttaacaa aacattttgt ttcaattcag 5364
tttgcatcgc aataaatctc tactagagac attttttatac agcatagtat tatacaacac 5424
attcaaaata aggatatttt tatccacctt taaaataagt aaaaaactgc tttggtataa 5484
caccataatg tttattaaaa accctaataa aataagatgt actggaaatt ccaatcatat 5544
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tcaattgcat taagaactgg ttaaaattag tattctcaga ttctagtctt tttctgatgg 5664
ttatttctga ttcattaaac atatctgcaa tgatagccag tgtccatttt ctggatagat 5724
cttttctgat aatatttctg accttgtcag aaaaaaattc acagatgata tataaattga 5784
ttctatta ttt ttt att att ctc gat ctt tga aat taa ata tat caa att 5834
         Phe Phe Ile Ile Leu Asp Leu  *  Asn  *  Ile Tyr Gln Ile
             1625              1630                        1635


aga tat aaa agc tga gtc atc ata gct att tat att ttt taa tac atc   5882
Arg Tyr Lys Ser  *  Val Ile Ile Ala Ile Tyr Ile Phe  *  Tyr Ile
             1640              1645                        1650


cag taa ggt ttt atc cac ttc tgt ttt cat tat ttt cct tga cat att   5930
Gln  *  Gly Phe Ile His Phe Cys Phe His Tyr Phe Pro  *  His Ile
             1655              1660


tct aca atc att ggt atc tat ttt tga cat acc ata tat tat cat caa   5978
Ser Thr Ile Ile Gly Ile Tyr Phe  *  His Thr Ile Tyr Tyr His Gln
```

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tgc atc ctt taa atg tct tag tat gtc tcc gtt caa tct gaa tgc aac   6026
Cys Ile Leu  *  Met Ser  *  Tyr Val Ser Val Gln Ser Glu Cys Asn
1680                          1685                1690
```

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ata tgg ttt ttc tga taa aat ttg ctt ctg tat tct tac aga tat att   6074
Ile Trp Phe Phe  *   *  Asn Leu Leu Leu Tyr Ser Tyr Arg Tyr Ile
    1695                          1700                1705
```

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cac ccc tct ttc aag aaa tac agg t gatgctgcca acttactgat           6119
His Pro Ser Phe Lys Lys Tyr Arg
            1710                  1715
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ttagtgtatg atggtgtttt tgaggtgctc cagtggcttc tgtttctatc agctgtccct 6179
cctgttcagc tactgacggg gtggtgcgta acggcaaaag cactgccgga catcagcgct 6239
atctctgctc tcactgccgt aaaacatggc aactgcagtt cacttacact gcttctcaac 6299
ccggtacgca ccagaaaatc attgatatgg ccatgaatgg cgttggatgc cgggcaacag 6359
cccgcattat gggcgttggc ctcaacacga ttttacgtca cttaaaaaac tcaggccgca 6419
gtcggtaacc tcgcgcatac agccgggcag tgacgtcatc gtctgcgcgg aaatggacga 6479
acagtggggc tatgtcgggg ctaaatcgcg ccagcgctgg ctgttttacg cgtatgacag 6539
gctccggaag acggttgttg cgcacgtatt cggtgaacgc actatggcga cgctggggcg 6599
tcttatgagc ctgctgtcac cctttgacgt ggtgatatgg atgacggatg ctggccgct  6659
gtatgaatcc cgcctgaagg gaaagctgca cgtaatcagc aagcgatata cgcagcgaat 6719
tgagcggcat aacctgaatc tgaggcagca cctggcacgg ctgggacgga agtcgctgtc 6779
gttctcaaaa tcggtggagc tgcatgacaa agtcatcggg cattatctga acataaaaca 6839
ctatcaataa gttagagtca ttacctggtt cacgtattat tatccgtgac tctttcctgg 6899
taactcccgc ataataacct cacttttcca gtattccaga agatgatgtt ttttcctcga 6959
taataaaaat gtgccaatat ggaaataaga aatcggattt tttatcagca tacgcaaatt 7019
ttcagataac aatgaataca gatgtatttt atatacacag ataaaaccgc gcaacagaca 7079
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ttttttagct atagtattat tggttttacc tattttcgtg attgtgtttc tgtatatttg 7199
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Leu Phe Thr Phe Ala Val Ser Ala Asp Lys Ile Pro Gly Asp Glu Ser
            20                  25                  30
Ile Thr Asn Ile Phe Gly Pro Arg Asp Arg Asn Glu Ser Ser Pro Lys
        35                  40                  45
His Asn Ile Leu Asn Asn His Ile Thr Ala Tyr Ser Glu Ser His Thr
    50                  55                  60
Leu Tyr Asp Arg Met Thr Phe Leu Cys Leu Ser Ser His Asn Thr Leu
65                  70                  75                  80
Asn Gly Ala Cys Pro Thr Ser Glu Asn Pro Ser Ser Ser Ser Val Ser
                85                  90                  95
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Gly Glu Thr Asn Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile
        100                 105                 110
Lys Arg Glu Leu Gln Ile Lys Gly Tyr Lys Gln Leu Leu Phe Lys Ser
        115                 120                 125
Val Asn Cys Pro Ser Gly Leu Thr Leu Asn Ser Ala His Phe Asn Cys
        130                 135                 140
Asn Lys Asn Ala Ala Ser Gly Ala Ser Leu Tyr Leu Tyr Ile Pro Ala
145                 150                 155                 160
Gly Glu Leu Lys Asn Leu Pro Phe Gly Gly Ile Trp Asp Ala Thr Leu
                165                 170                 175
Lys Leu Arg Val Lys Arg Arg Tyr Ser Glu Thr Tyr Gly Thr Tyr Thr
                180                 185                 190
Ile Asn Ile Thr Ile Lys Leu Thr Asp Lys Gly Asn Ile Gln Ile Trp
                195                 200                 205
Leu Pro Gln Phe Lys Ser Asp Ala Arg Val Asp Leu Asn Leu Arg Pro
        210                 215                 220
Thr Gly Gly Gly Thr Tyr Ile Gly Arg Asn Ser Val Asp Met Cys Phe
225                 230                 235                 240
Tyr Asp Gly Tyr Ser Thr Asn Ser Ser Ser Leu Glu Ile Arg Phe Gln
                245                 250                 255
Asp Asn Asn Pro Lys Ser Asp Gly Lys Phe Tyr Leu Arg Lys Ile Asn
                260                 265                 270
Asp Asp Thr Lys Glu Ile Ala Tyr Thr Leu Ser Leu Leu Leu Ala Gly
        275                 280                 285
Ser Leu Thr Pro Thr Asn Gly Thr Ser Leu Asn Ile Ala Asp Ala Ala
        290                 295                 300
Ser Leu Phe Thr Asn Trp Asn Arg Ile Thr Ala Val Thr Met Pro Glu
305                 310                 315                 320
Ile Ser Val Pro Val Leu Cys Trp Pro Gly Arg Leu Gln Leu Asp Ala
                325                 330                 335
Lys Val Glu Asn Pro Glu Ala Gly Gln Tyr Met Gly Asn Ile Asn Val
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Thr Phe Thr Pro Ser Ser Gln Thr Leu
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<210> 29
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<223> ETEC Protein Homology Sequence

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            20                  25                  30
Thr Asn Thr Ile Gly Pro His Asp Arg Gly Gly Ser Ser Pro Ile Tyr
        35                  40                  45
Asn Ile Leu Asn Ser Tyr Leu Thr Ala Tyr Asn Gly Ser His His Leu
    50                  55                  60
Tyr Asp Arg Met Ser Phe Leu Cys Leu Ser Ser Gln Asn Thr Leu Asn
65                  70                  75                  80
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Gly Ala Cys Pro Ser Ser Asp Ala Pro Gly Thr Ala Thr Ile Asp Gly
                    85   90   95
Glu Thr Asn Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys
                100   105   110
Arg Glu Leu Gln Ile Lys Gly Tyr Lys Gln Phe Leu Phe Lys Asn Ala
                115   120   125
Asn Cys Pro Ser Lys Leu Ala Leu Asn Ser Ser His Phe Gln Cys Asn
                130   135   140
Arg Glu Gln Ala Ser Gly Ala Thr Leu Ser Leu Tyr Ile Pro Ala Gly
145   150   155   160
Glu Leu Asn Lys Leu Pro Phe Gly Gly Val Trp Asn Ala Val Leu Lys
                165   170   175
Leu Asn Val Lys Arg Arg Tyr Thr Thr Tyr Gly Thr Tyr Thr Ile Asn
                180   185   190
Ile Thr Val Asn Leu Thr Asp Lys Gly Asn Ile Gln Ile Trp Leu Pro
                195   200   205
Gln Phe Lys Ser Asn Ala Arg Val Asp Leu Asn Leu Arg Pro Thr Gly
    210   215   220
Gly Gly Thr Tyr Ile Gly Arg Asn Ser Val Asp Met Cys Phe Tyr Asp
225   230   235   240
Gly Tyr Ser Thr Met Ser Ser Ser Leu Glu Ile Arg Phe Gln Asp Asp
                    245   250   255
Asn Ser Lys Ser Asp Gly Lys Phe Tyr Leu Lys Lys Ile Asn Asp Asp
                260   265   270
Ser Lys Glu Leu Val Tyr Thr Leu Ser Leu Leu Leu Ala Gly Lys Asn
                275   280   285
Leu Thr Pro Thr Asn Gly Gln Ala Leu Asn Ile Asn Thr Ala Ser Leu
                290   295   300
Glu Thr Asn Trp Asn Arg Ile Thr Ala Val Thr Met Pro Glu Ile Ser
305   310   315   320
Val Pro Val Leu Cys Trp Pro Gly Arg Leu Gln Leu Asp Ala Lys Val
                325   330   335
Lys Asn Pro Glu Ala Gly Gln Tyr Met Gly Asn Ile Lys Ile Thr Phe
                340   345   350
Thr Pro Ser Ser Gln Thr Leu
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<220>
<223> ETEC Protein Homology Sequence

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                20   25   30
Thr Phe Ser Ile Gly Pro Ile Asp Arg Ser Ala Ala Ala Ser Tyr Pro
            35   40   45
Ala His Tyr Ile Phe His Glu Asx Val Ala Gly Tyr Asn Lys Asp His
        50   55   60

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Ser Leu Phe Asp Arg Met Thr Phe Leu Cys Met Ser Ser Thr Asp Ala
65                  70              75                  80
Ser Lys Gly Ala Cys Pro Thr Gly Glu Asn Ser Lys Ser Ser Gln Gly
                85              90                  95
Glu Thr Asn Ile Lys Leu Ile Phe Thr Glu Lys Lys Ser Leu Ala Arg
            100             105             110
Lys Thr Leu Asn Leu Lys Gly Tyr Lys Arg Phe Leu Tyr Glu Ser Asp
        115             120             125
Arg Cys Ile His Tyr Val Asp Lys Met Asn Leu Asn Ser His Thr Val
    130             135             140
Lys Cys Val Gly Ser Phe Thr Arg Gly Val Asp Phe Thr Leu Tyr Ile
145             150             155                 160
Pro Gln Gly Glu Ile Asp Gly Leu Leu Thr Gly Gly Ile Trp Lys Ala
            165             170             175
Thr Leu Glu Leu Arg Val Lys Arg His Tyr Asp Tyr Asn His Gly Thr
        180             185             190
Tyr Lys Val Asn Ile Thr Val Asp Leu Thr Asp Lys Gly Asn Ile Gln
        195             200             205
Val Trp Thr Pro Lys Phe His Ser Asp Pro Arg Ile Asp Leu Asn Leu
    210             215             220
Arg Pro Glu Gly Asn Gly Lys Tyr Ser Gly Ser Asn Val Leu Glu Met
225             230             235                 240
Cys Leu Tyr Asp Gly Tyr Ser Thr His Ser Gln Ser Ile Glu Met Arg
            245             250             255
Phe Gln Asp Asp Ser Gln Thr Gly Asn Asn Glu Tyr Asn Leu Ile Lys
            260             265             270
Thr Gly Glu Pro Leu Lys Lys Leu Pro Tyr Lys Leu Ser Leu Leu Leu
            275             280             285
Gly Gly Arg Glu Phe Tyr Pro Asn Asn Gly Lys Ala Phe Thr Ile Asn
    290             295             300
Asp Thr Ser Ser Leu Phe Ile Asn Trp Asn Arg Ile Lys Ser Val Ser
305             310             315                 320
Leu Pro Gln Ile Ser Ile Pro Val Leu Cys Trp Pro Ala Asn Leu Thr
            325             330             335
Phe Met Ser Glu Leu Asn Asn Pro Glu Ala Gly Glu Tyr Ser Gly Ile
        340             345             350
Leu Asn Val Thr Phe Thr Pro Ser Ser Ser Ser Leu
        355             360


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            20              25              30
Phe Gln Ala Pro Arg Leu Asp Arg Ser Val Gln Ser Pro Ile Tyr Asn
        35              40              45
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Ile Phe Thr Asn His Val Ala Gly Tyr Ser Leu Ser His Ser Leu Tyr
    50                  55                  60
Asp Arg Ile Val Phe Leu Cys Thr Ser Ser Asn Pro Val Asn Gly
65                  70                  75                  80
Ala Cys Pro Thr Ile Gly Thr Ser Gly Val Gln Tyr Gly Thr Thr Thr
                85                  90                  95
Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys Arg Asn Ile
                100                 105                 110
Asn Ile Ala Gly Asn Lys Lys Pro Ile Trp Glu Asn Gln Ser Cys Asp
            115                 120                 125
Phe Ser Asn Ile Met Val Leu Asn Ser Lys Ser Trp Ser Cys Gly Ala
    130                 135                 140
His Gly Asn Ala Asn Gly Thr Ile Leu Asn Leu Tyr Ile Pro Ala Gly
145                 150                 155                 160
Glu Ile Asn Lys Leu Pro Phe Gly Gly Ile Trp Glu Ala Thr Leu Ile
                165                 170                 175
Leu Arg Leu Ser Arg Tyr Gly Glu Val Ser Ser Thr His Tyr Gly Asn
                180                 185                 190
Tyr Thr Val Asn Ile Thr Val Asp Leu Thr Asp Lys Gly Asn Ile Gln
                195                 200                 205
Val Trp Leu Pro Gly Phe His Ser Asn Pro Arg Val Asp Leu Asn Leu
    210                 215                 220
Arg Pro Ile Gly Asn Tyr Lys Tyr Ser Gly Ser Asn Ser Leu Asp Met
225                 230                 235                 240
Cys Phe Tyr Asp Gly Tyr Ser Thr Asn Ser Asp Ser Met Val Ile Lys
                245                 250                 255
Phe Gln Asp Asp Asn Pro Thr Asn Ser Ser Glu Tyr Asn Leu Tyr Lys
                260                 265                 270
Ile Gly Gly Thr Glu Lys Leu Pro Tyr Ala Val Ser Leu Ile Gly Glu
                275                 280                 285
Lys Ile Phe Tyr Pro Val Asn Gly Gln Ser Phe Thr Ile Asn Asp Ser
    290                 295                 300
Ser Val Leu Glu Thr Asn Trp Asn Arg Val Thr Ala Val Ala Met Pro
305                 310                 315                 320
Glu Val Asn Val Pro Val Leu Cys Trp Pro Ala Arg Leu Leu Leu Asn
                325                 330                 335
Ala Asp Val Asn Ala Pro Asp Ala Gly Gln Tyr Ser Gly Gln Ile Tyr
                340                 345                 350
Ile Thr Phe Thr Pro Ser Val Glu Asn Leu
        355                 360


<210> 32
<211> 353
<212> PRT
<213> Artificial Sequence

<220>
<223> ETEC Protein Homology Sequence

<400> 32
Met Ser Asn Ile Cys Lys Trp Thr Ser Met Thr Ala His Trp Ser Ala
1                   5                   10                  15
Ile Ile Asn Phe Ile Arg Lys Tyr Val Tyr Pro Ala Arg Ile Ile Ala
                20                  25                  30
```

```
Ile Leu Ala Gly Ala Thr Leu Pro Gln Val Ala Asp Ala Ile Thr Val
        35                  40                  45
Asp Leu Asn Tyr Asp Lys Asn Asn Val Ala Val Ile Thr Pro Val Trp
    50                  55                  60
Ser Gln Glu Trp Ser Val Ala Asn Val Leu Gly Gly Trp Val Cys Arg
65                  70                  75                  80
Ser Asn Arg Asn Glu Asn Glu Gly Cys Glu Glu Thr His Leu Val Trp
                85                  90                  95
Trp Tyr Ala Phe Gly Ala Tyr Ser Ile Arg Leu Arg Phe Arg Glu Gln
                100                 105                 110
Ile Ser His Ala Glu Ile Thr Leu Ile Leu Leu Gly Ser Val Arg Asp
        115                 120                 125
Ala Cys Thr Gly Val Ile Asn Met Asn Ala Ala Ala Cys Gln Trp Gly
    130                 135                 140
Arg Ser Leu Lys Leu Arg Ile Pro Ser Glu Glu Leu Ala Lys Ile Pro
145                 150                 155                 160
Thr Ser Gly Thr Trp Lys Ala Thr Leu Val Leu Asp Tyr Leu Gln Trp
                165                 170                 175
Gly Gly Asp Asp Pro Leu Gly Thr Ser Thr Asp Ile Thr Leu Asn
                180                 185                 190
Val Thr Asp His Phe Ala Glu Asn Ala Ala Ile Tyr Phe Pro Gln Phe
        195                 200                 205
Gly Thr Ala Thr Pro Arg Val Asp Leu Asn Leu His Arg Met Asn Ala
        210                 215                 220
Ser Gln Met Ser Gly Arg Ala Asn Leu Asp Met Cys Leu Tyr Asp Gly
225                 230                 235                 240
Gly Val Lys Ala Arg Ser Leu Gln Met Met Glu Gly Ser Asn Lys Ser
                245                 250                 255
Gly Thr Gly Phe Gln Val Ile Lys Ser Asp Ser Ala Asp Thr Ile Asp
                260                 265                 270
Tyr Ala Val Ser Met Asn Tyr Gly Gly Arg Ser Ile Pro Val Thr Arg
        275                 280                 285
Gly Val Glu Phe Ser Leu Asp Asn Val Asp Lys Ala Ala Thr Arg Pro
        290                 295                 300
Val Val Leu Pro Gly Gln Arg Gln Ala Val Arg Cys Val Pro Val Pro
305                 310                 315                 320
Leu Thr Leu Thr Thr Gln Pro Phe Asn Ile Arg Glu Lys Arg Ser Gly
                325                 330                 335
Glu Tyr Gln Gly Thr Leu Thr Val Thr Met Leu Met Gly Thr Gln Thr
                340                 345                 350
Pro
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<210> 33
<211> 165
<212> PRT
<213> Artificial Sequence

<220>
<223> ETEC Protein Homology Sequence

<400> 33
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Met Lys Leu Lys Lys Thr Ile Gly Ala Met Ala Leu Thr Thr Met Phe
 1               5                   10                  15
```

```
Val Ala Met Ser Ala Ser Ala Val Glu Lys Asn Ile Thr Val Thr Ala
                20                  25                  30
Ser Val Asp Pro Thr Ile Asp Ile Leu Gln Ala Asp Gly Ser Ser Leu
            35                  40                  45
Pro Thr Ala Val Glu Leu Thr Tyr Ser Pro Ala Ala Ser Arg Phe Glu
        50                  55                  60
Asn Tyr Lys Ile Ala Thr Lys Val His Thr Asn Val Ile Asn Lys Asn
65                  70                  75                  80
Val Leu Val Lys Leu Val Asn Asp Pro Lys Leu Thr Asn Val Leu Asp
                85                  90                  95
Ser Thr Lys Gln Leu Pro Ile Thr Val Ser Tyr Gly Gly Lys Leu Ser
                100                 105                 110
Thr Ala Asp Val Thr Phe Glu Pro Ala Glu Leu Asn Phe Gly Thr Ser
            115                 120                 125
Gly Val Thr Gly Val Ser Ser Ser Gln Asp Leu Val Ile Gly Ala Thr
            130                 135                 140
Thr Ala Gln Ala Pro Ser Ala Asn Tyr Ser Gly Val Val Ser Ile Leu
145                 150                 155                 160
Met Thr Leu Ala Ser
                165


<210> 34
<211> 168
<212> PRT
<213> Artificial Sequence

<220>
<223> ETEC Protein Homology Sequence

<400> 34
Met Lys Phe Lys Lys Thr Ile Gly Ala Met Ala Leu Thr Thr Met Phe
1                   5                   10                  15
Val Ala Val Ser Ala Ser Ala Val Glu Lys Asn Ile Thr Val Thr Ala
                20                  25                  30
Ser Val Asp Pro Ala Ile Asp Leu Leu Gln Ala Asp Gly Asn Ala Leu
            35                  40                  45
Pro Ser Val Lys Leu Ala Tyr Ser Pro Ala Ser Lys Ile Phe Glu Ser
        50                  55                  60
Tyr Arg Val Met Thr Gln Val His Thr Asn Asp Ala Thr Lys Lys Val
65                  70                  75                  80
Ile Val Lys Leu Ala Asp Thr Pro Gln Leu Thr Asp Val Leu Asn Ser
                85                  90                  95
Thr Val Gln Met Pro Ile Ser Val Ser Trp Gly Gly Val Leu Ser Thr
                100                 105                 110
Thr Ala Lys Glu Phe Glu Ala Ala Ala Leu Gly Tyr Ser Ala Ser Gly
            115                 120                 125
Val Asn Gly Val Ser Ser Ser Gln Glu Leu Val Ile Ser Ala Ala Pro
            130                 135                 140
Lys Thr Ala Gly Thr Ala Pro Thr Ala Gly Asn Tyr Ser Gly Val Val
145                 150                 155                 160
Ser Leu Val Met Thr Leu Gly Ser
                165
```

<210> 35
<211> 170
<212> PRT
<213> Artificial Sequence

<220>
<223> ETEC Protein Homology Sequence

<400> 35
Met Lys Leu Lys Lys Thr Ile Gly Ala Met Ala Leu Ala Thr Leu Phe
1   5   10   15
Ala Thr Met Gly Ala Ser Ala Val Glu Lys Thr Ile Ser Val Thr Ala
                20   25   30
Ser Val Asp Pro Thr Val Asp Leu Leu Gln Ser Asp Gly Ser Ala Leu
            35   40   45
Pro Asn Val Ala Leu Thr Tyr Ser Pro Ala Val Asn Asn Phe Glu Ala
        50   55   60
His Thr Ile Asn Thr Val Val His Thr Asn Asp Ser Asp Lys Gly Val
65   70   75   80
Val Val Lys Leu Ser Ala Asp Pro Val Leu Ser Asn Val Leu Asn Pro
                85   90   95
Thr Leu Gln Ile Pro Val Ser Val Asn Phe Ala Gly Lys Pro Leu Ser
                100   105   110
Thr Thr Gly Ile Thr Ile Asp Ser Asn Asp Leu Asn Phe Ala Ser Ser
            115   120   125
Gly Val Asn Tyr Val Ser Ser Thr Gln Lys Leu Ser Ile His Ala Asp
        130   135   140
Ala Thr Arg Val Thr Gly Gly Ala Leu Thr Ala Gly Gln Tyr Gln Gly
145   150   155   160
Leu Val Ser Ile Ile Leu Thr Lys Ser Thr
                165   170

<210> 36
<211> 170
<212> PRT
<213> Artificial Sequence

<220>
<223> ETEC Protein Homology Sequence

<400> 36
Met Lys Leu Asn Lys Ile Ile Gly Ala Leu Val Leu Ser Ser Thr Phe
1   5   10   15
Val Ser Met Gly Ala Ser Ala Ala Glu Lys Asn Ile Thr Val Thr Ala
                20   25   30
Ser Val Asp Pro Thr Ile Asp Leu Met Gln Ser Asp Gly Thr Ala Leu
            35   40   45
Pro Ser Ala Val Asn Ile Ala Tyr Leu Pro Gly Glu Lys Arg Phe Glu
        50   55   60
Ser Ala Arg Ile Asn Thr Gln Val His Thr Asn Asn Lys Thr Lys Gly
65   70   75   80
Ile Gln Ile Lys Leu Thr Asn Asp Asn Val Val Met Thr Asn Leu Ser
                85   90   95
Asp Pro Ser Lys Thr Ile Pro Leu Glu Val Ser Phe Ala Gly Thr Lys

```
                   100                      105                       110
Leu Ser Thr Ala Ala Thr Ser Ile Thr Ala Asp Gln Leu Asn Phe Gly
        115                      120                       125
Ala Ala Gly Val Glu Thr Val Ser Ala Thr Lys Glu Leu Val Ile Asn
    130                      135                       140
Ala Gly Ser Thr Gln Gln Thr Asn Ile Val Ala Gly Asn Tyr Gln Gly
145                      150                       155                       160
Leu Val Ser Ile Val Leu Thr Gln Glu Pro
                   165                      170
```

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<210> 37
<211> 168
<212> PRT
<213> Artificial Sequence

<220>
<223> ETEC Protein Homology Sequence

<400> 37
Met Lys Leu Lys Tyr Thr Ile Gly Ala Met Ala Leu Ser Thr Ile Phe
1               5                       10                      15
Val Ala Val Ser Ala Ser Ala Val Glu Lys Asn Ile Thr Val Thr Ala
            20                      25                      30
Ser Val Asp Pro Thr Ile Asp Ile Leu Gln Ala Asn Gly Ser Ala Leu
            35                      40                      45
Pro Thr Ala Val Asp Leu Thr Tyr Leu Pro Gly Ala Lys Thr Phe Glu
        50                      55                      60
Asn Tyr Ser Val Leu Thr Gln Ile Tyr Thr Asn Asp Pro Ser Lys Gly
65                      70                      75                      80
Leu Asp Val Arg Leu Val Asp Thr Pro Lys Leu Thr Asn Ile Leu Gln
                    85                      90                      95
Pro Thr Ser Thr Ile Pro Leu Thr Val Ser Trp Ala Gly Arg Thr Leu
                100                     105                     110
Ser Thr Ser Ala Gln Lys Ile Ala Val Gly Asp Leu Gly Phe Gly Ser
            115                     120                     125
Thr Gly Thr Ala Gly Val Ser Asn Ser Lys Glu Leu Val Ile Gly Ala
        130                     135                     140
Thr Thr Ser Gly Lys Pro Ser Ala Gly Lys Tyr Gln Gly Val Val Ser
145                     150                     155                     160
Ile Val Met Thr Gln Ser Thr Asn
                    165
```

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<210> 38
<211> 142
<212> PRT
<213> Artificial Sequence

<220>
<223> ETEC Protein Homology Sequence

<400> 38
Val Asp Pro Thr Ile Asp Ile Leu Gln Ala Asn Gly Ser Ala Leu Pro
1               5                       10                      15
```

```
Thr Ala Val Asp Leu Thr Tyr Leu Pro Gly Ala Lys Thr Phe Glu Asn
            20                  25                  30
Tyr Ser Val Leu Thr Gln Ile Tyr Thr Asn Asp Pro Ser Lys Gly Leu
            35                  40                  45
Asp Val Arg Leu Val Asp Thr Pro Lys Leu Thr Asn Ile Leu Gln Pro
        50                  55                  60
Thr Ser Thr Ile Pro Leu Thr Val Ser Trp Ala Gly Lys Thr Leu Ser
65                  70                  75                  80
Thr Ser Ala Gln Lys Ile Ala Val Gly Asp Leu Gly Phe Gly Ser Thr
                85                  90                  95
Gly Thr Ala Gly Val Ser Asn Ser Lys Glu Leu Val Ile Gly Ala Thr
            100                 105                 110
Thr Ser Gly Thr Ala Pro Ser Ala Gly Lys Tyr Gln Gly Val Val Ser
        115                 120                 125
Ile Val Met Thr Gln Ser Thr Asp Thr Ala Ala Pro Val Pro
    130                 135                 140


<210> 39
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> ETEC Protein Homology Sequence

<400> 39
Val Asp Pro Lys Leu Asp Leu Leu Gln Ala Asp Gly Thr Ser Leu Pro
 1               5                  10                  15
Asp Ser Ile Ala Leu Thr Tyr Ser Ser Ala Ser Asn Asn Phe Glu Val
            20                  25                  30
Tyr Ser Leu Asn Thr Ala Ile His Thr Asn Asp Lys Thr Lys Ala Val
            35                  40                  45
Val Val Lys Leu Ser Ala Pro Ala Val Leu Ser Asn Ile Met Lys Pro
        50                  55                  60
Ser Ser Gln Ile Pro Met Lys Val Thr Leu Gly Gly Lys Thr Leu Ser
65                  70                  75                  80
Thr Ala Asp Ala Glu Phe Ala Ala Asp Thr Leu Asn Phe Gly Ala Ser
                85                  90                  95
Gly Val Glu Asn Val Ser Ser Val Gln Gln Leu Thr Ile His Ala Glu
            100                 105                 110
Ala Ala Pro Pro Glu Ala Gly Asn Tyr Gln Gly Val Ile Ser Leu Ile
        115                 120                 125
Met Thr Gln Lys Thr
    130


<210> 40
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> ETEC Protein Homology Sequence
```

<400> 40

Val Asp Pro Lys Leu Asp Leu Leu Gln Ala Asp Gly Thr Ser Leu Pro
1   5   10   15
Asp Ser Ile Ala Leu Thr Tyr Ser Ser Ala Ser Asn Asn Phe Glu Val
            20   25   30
Tyr Ser Leu Asn Thr Ala Ile His Thr Asn Asp Lys Ser Lys Gly Val
        35   40   45
Val Val Lys Leu Ser Ala Ser Pro Val Leu Ser Asn Ile Met Pro Asn
    50   55   60
Ser Gln Ile Pro Met Lys Val Thr Leu Gly Gly Glu Thr Leu Asn Thr
65   70   75   80
Thr Asp Thr Glu Phe Thr Val Asp Thr Leu Asn Phe Gly Thr Ser Gly
                85   90   95
Val Glu Asn Val Ser Ser Thr Gln Gln Leu Thr Ile His Ala Asp Thr
                100   105   110
Gln Gly Thr Ala Pro Glu Ala Gly Asn Tyr Gln Gly Ile Ile Ser Leu
        115   120   125
Ile Met Thr Gln Lys Thr
        130